NO:49, GenBank #U32720) were aligned using the ClustalX alignment program (Thompson *et al.* (1997) *Nucleic Acids Res.* **25,** 4876-82). The shading was produced by the program GeneDoc (Nicholas, K. B., and Nicholas, H. B. (1997) ~~URL: http://www.cris.com/~ketchup/genedoc.shtml~~ www.cris.com/~ketchup/genedoc.shtml).

Please replace the paragraph beginning at page15, line 11 with the following amended paragraph:

Examples of algorithms that are suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul *et al.* (1990) *J. Mol. Biol.* 215: 403-410 and Altschuel *et al.* (1977) *Nucleic Acids Res.* 25: 3389-3402, respectively. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information ~~(http://www.ncbi.nlm.nih.gov/)~~ (www.ncbi.nlm.nih.gov/). For example, the comparisons can be performed using a BLASTN Version 2.0 algorithm with a wordlength (W) of 11, G=5, E=2, q= -2, and r = 1., and a comparison of both strands. For amino acid sequences, the BLASTP Version 2.0 algorithm can be used, with the default values of wordlength (W) of 3, G=11, E=1, and a BLOSUM62 substitution matrix. (*see* Henikoff & Henikoff, *Proc. Natl. Acad. Sci. USA* 89:10915 (1989)).

1/23/07 TM

Please replace the paragraph beginning at page ~~49~~ 48, line 2 with the following amended paragraph:

The primers used to amplify the LPS biosynthesis locus of *C. jejuni* OH4384 were based on preliminary sequences available from the website ~~(URL: http://www.sanger.ac.uk/Projects/C_jejuni/)~~ ~~(www.sanger.ac.uk/Projects/C_jejuni/)~~ of the *C. jejuni* sequencing group (Sanger Centre, UK) who sequenced the complete genome of the strain NCTC11168. The primers CJ-42 and CJ-43 (all primers sequences are described in Table 2) were used to amplify an 11.47 kb locus using the Expand™ long template PCR system. The PCR product was purified on a S-300 spin column (Pharmacia Biotech) and completely sequence on